FIGURE 6A

1. 'A' Allele, CYP2D6'3, A21337 deletion, Frameshift resulting in zero enzyme activity

	2637	
SEQ ID NO:6	5'- GCTAACTGAGCACAGGATGACC -3' NH2	CYPwt(+)A2624, 22mer,54%GC, Tm=63-64C
SEQ ID NO:7	5'- GCTAACTGAGCACAGGATGACC(A)30 -3' NH2	CYPwt(+)A2624 (A)30-3'NH2
SEQ ID NO:8	5'- CTAACTGAGCACAGGATGACC(A)30 -3' NH2	CYPwt(+)A2625 (A)30-3'NH2
SEQ ID NO:9	5'- CTAACTGAGCACAGGATGAC(A)30 -3' NH2	CYPwt(+)A2625b (A)30-3'NH2
SEQ ID NO:10	5'- GCTAACTGAGCAC-GGATGACC -3'NH2	CYPmut(+)A2624,21 mer,57%GC, Tm=61-63C
SEQ ID NO:11	5'- GCTAACTGAGCAC-GGATGACC(A)30 -3' NH2	CYPmut(+)A2624 (A)30-3'NH2
SEQ ID NO:12	5'- CTAACTGAGCAC-GGATGACC(A)30 -3' NH2	CYPmut(+)A2625 (A)30-3'NH2
SEQ ID NO:13	5'- CTAACTGAGCAC-GGATGAC(A)30 -3' NH2	CYPmut(+)A2625b(A)30-3'NH2
	|-2612	
SEQ ID NO:14	5'- GCTGGATGAGCTGCTAACTGAGCACAGGATGACCTGGGACCCAGCCCAGCC -3'	Wild Type(+)
SEQ ID NO:15	5'- GCTGGATGAGCTGCTAACTGAGCAC-GGATGACCTGGGACCCAGCCCAGCC -3'	Mut(+)

2. 'B' Allele, CYP2D6*4, G1934A, Spliceing defect resulting in zero enzyme activity

A. wt Probe - CYPwt(-)B1922 (C/A to mut at base 5) & CYPmut(+)B1922 (A/C to mut at base 13)

	1934	
SEQ ID NO:16	NH2 3'- GAGGGTGGGGGTCCTGC -5'	CYPwt(-)B1922, 17mer,76%GC, Tm=66C
SEQ ID NO:17	5'- CTCCCACCCCCAGGACG -3'NH2	CYPwt(+)B1922-Target
SEQ ID NO:18	5'- CTCCCACCCCCAAGACG -3' NH2	CYPmut(+)B1922, 17mer,71%GC, Tm=58-60C
SEQ ID NO:19	NH2 3'- GAGGGTGGGGGTTCTGC -5'	CYPmut(-)B1922- Target
	|-1909	
SEQ ID NO:20	5' - CCCTTACCCGCATCTCCCACCCCCAGGACGCCCCTTTCGCCCCAACGGTCT -3'	WildType(+)
SEQ ID NO:21	5 '- CCCTTACCCGCATCTCCCACCCCCAAGACGCCCCTTTCGCCCCAACGGTCT -3'	Mut(+)

B. CYPwt(-)B1930 (C/A to mut at base 13) and CYPmut(+)B1930 (A/C to wt at base 5)

SEQ ID NO:22	NH2 3'- GGGTCCTGCGGGGAAAG -5'	CYPwt(-) B1930,17mer,71%GC, Tm=56C
SEQ ID NO:23	NH2 3'- (A)30GGGTCCTGCGGGGAAAG -5'	CYPwt(-) B1930(A)30-3'NH2
SEQ ID NO:24	5'- CCCAAGACGCCCCTTTC -3' NH2	CYPmut(+)B1930, 17mer,65%GC,Tm=54C
SEQ ID NO:25	5'- CCCAAGACGCCCCTTTC(A)30 -3' NH2	CYPmut(+)B1930 (A)30-3'NH2
	|-1909	
SEQ ID NO:26	5'- CCCTTACCCGCATCTCCCACCCCCAGGACGCCCCTTTCGCCCCAACGGTCT -3'	Wild Type(+)
SEQ ID NO:27	5'- CCCTTACCCGCATCTCCCACCCCCAAGACGCCCCTTTCGCCCCAACGGTCT -3'	Mut(+)

FIGURE 6B

3. 'C' Allele, CYP2D6*9, G2702-A2704 deletion, decreased enzyme activity

```
                                                |-2702
SEQ ID NO:28                5'- GCAGAGATGGAGAAGGTGAGAG -3'NH2            CYPwt(+)C2691, 22mer,55%GC, Tm=60C
SEQ ID NO:29                5'- GCAGAGATGGAGAAGGTGAGAG(A)30 -3' NH2      CYPwt(+)C2691 (A)30-3'NH2
SEQ ID NO:30                 5'- CAGAGATGGAGAAGGTGAGAG(A)30 -3' NH2      CYPwt(+)C2692 (A)30-3'NH2
SEQ ID NO:31                5'- GCAGAGATGGA---GGTGAGAGTG -3' NH2         CYPmut(+)C2691, 21mer, 57%GC, Tm=60C
SEQ ID NO:32                5'- GCAGAGATGGA---GGTGAGAGTG(A)30 -3' NH2    CYPmut(+)C2691 (A)30-3'NH2
SEQ ID NO:33                 5'- CAGAGATGGA---GGTGAGAGTG(A)30 -3' NH2    CYPmut(+)C2692 (A)30-3'NH2
              |-2676
SEQ ID NO:34  3'- TGACTCCGGAAGGACCGTCTCTACCTCTTCCACTCTCACCGACGGTGCCAC -5'  Wild Type(-)
SEQ ID NO:35  3'- TGACTCCGGAAGGACCGTCTCTACCT---CCACTCTCACCGACGGTGCCAC -5'  Mut (-)
```

4. 'E' Allele, CYP2D6*7, A3023C, H324P amino acid change results in zero enzyme activity

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+)E3009 (C/A to wt at base 15)

```
                                    3023
SEQ ID NO:36          NH2 3'- CGAGTACTAGGATGTAGGC -5'                    CYPwt(-)E3009, 19mer,53%GC, Pred Tm=57
SEQ ID NO:37     NH2 3'- (A)30CGAGTACTAGGATGTAGGC -5'                    CYPwt(-) E3009(A)30-3'NH2
SEQ ID NO:38              5'- GCTCATGATCCTACCTCCG -3'NH2                  CYPmut(+)E3009,19mer,58%GC,Pred Tm=59C
SEQ ID NO:39              5'- GCTCATGATCCTACCTCCG(A)30 -3'NH2             CYPmut(+) E3009(A)30-3'NH2
              |-2998
SEQ ID NO:40  5'- TGGGGCCTCCTGCTCATGATCCTACATCCGGATGTGCAGC|GTGAGCCCATC -3'      Wild Type(+)
SEQ ID NO:41  5'- TGGGGCCTCCTGCTCATGATCCTACCTCCGGATGTGCAGC|GTGAGCCCATC -3'      Mut(+)
                                                         |-3038-Intron Start
```

B. CYPwt(-)E3018 (T/C to mut at base 14) and CYPmut(+)E3018 (C/T to wt at base 6)

```
SEQ ID NO:42                NH2 3'- GGATGTAGGCCTACACGTC -5'              CYPwt(-)E3018,19mer,58%GC,Tm=60
SEQ ID NO:43                    5'- CCTACATCCGGATGTGCAG -3'              CYPwt(+)E3018- Target
SEQ ID NO:44                    5'- CCTACCTCCGGATGTGCAG -3' NH2          CYPmut(+)E3018,19mer,63%GC,Tm=62C
SEQ ID NO:45                    3'- GGATGGAGGCCTACACGTC -5'              CYPmut(-) E3018- Target
              |-2998
SEQ ID NO:46  5'- TGGGGCCTCCTGCTCATGATCCTACATCCGGATGTGCAGC|GTGAGCCCATC -3'   Wild Type(+)
SEQ ID NO:47  5'- TGGGGCCTCCTGCTCATGATCCTACCTCCGGATGTGCAGC|GTGAGCCCATC -3'   Mut(+)
                                                         |-3038-Intron Start
```

FIGURE 6C

5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity

```
                                        1846
SEQ ID NO:48                5'- CACTCCGGTGGGTGATGG(A)30 -3' NH2        CYPwt(+)G1840(A)30-3'NH2,18mer,67%GC, Tm=60
SEQ ID NO:49      NH2 3'- (A)30GTGAGGCCACCCACTACC -5'                  CYPwt(-) G1840(A)30-3'NH2
SEQ ID NO:50                5'- CACTCCTGTGGGTGATGG(A)30 -3' NH2        CYPmut(+)G1840(A)30-3'NH2,18mer, 61%GC, Tm=57
SEQ ID NO:51  5'- GTGCCGCCTTCGCCACTCC|GGTGGGTGATGGGCAGAAGGGCACAAAGCGGG -3'
SEQ ID NO:52  5'- GTGCCGCCTTCGCCACTCC|TGTGGGTGATGGGCAGAAGGGCACAAAGCGGG -3'
                           Exon 3 end-|-1846
```

6. 'T' Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity

```
SEQ ID NO:53              5'- GCTGGAGCAGTGGGTGAC -3' NH2                CYPwt(+)T1785, 18mer,67%GC, Trn=59-61C
SEQ ID NO:54              5'- GCTGGAGCAGTGGGTGAC(A)30 -3' NH2           CYPwt(+)T1785 (A)30-3'NH2
SEQ ID NO:55              5'-  CTGGAGCAGTGGGTGAC(A)30 -3' NH2           CYPwt(+)T1786 (A)30-3'NH2
SEQ ID NO:56              5'- GCTGGAGCAG-GGGTGAC -3' NH2                CYPmut(+)T1785, 17mer,71 %GC, Tm=58-60C
SEQ ID NO:57              5'- GCTGGAGCAG-GGGTGAC(A)30 -3' NH2           CYPmut(+)T1785 (A)30-3'NH2
SEQ ID NO:58               5'- CTGGAGCAG-GGGTGAC(A)30 -3' NH2           CYPmut(+)T1786 (A)30-3'NH2
                  |-1773
SEQ ID NO:59  5'-GGGCAAGAAGTCGCTGGAGCAGTGGGTGACCGAGGAGGCCGCCTGCCT -3'   Wild Type(+)
SEQ ID NO:60  5'-GGGCAAGAAGTCGCTGGAGCAG-GGGTGACCGAGGAGGCCGCCTGCCT -3'   Mut(+)
```

7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers were it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

```
SEQ ID NO:61       5'- GACCAGGGGGAGC-ATAGG(A)30-3' NH2          CYP2D6wt(+)1607(A)30-3'NH2
SEQ ID NO:62       5'- GACCTTGTGGAGCGCCAG(A)30-3' NH2           CYP2D7wt(+)1607(A)30-3'NH2
SEQ ID NO:63       5'- GACCAGGAAAAGC-ACAGG(A)30-3' NH2          CYP2D8wt(+)1607(A)30-3'NH2
SEQ ID NO:64       5'- GACCAGGAAAAGC-ACAGGG(A)30-3' NH2         CYP2D8wt(+) 1607b (A)30-3'NH2
                   |-1603
SEQ ID NO:65  5' - GGGAGACCAGGGGGAGC-ATAGGGTTGGAGTGGGTGGT -3'   2D6(+)
SEQ ID NO:66  5' - GGGAGACCTTGTGGAGCGCCAGGGTTGGAGTGGGTGGC -3'   2D7(+)
SEQ ID NO:67  5' - GGGAGACCAGGAAAAGC-ACAGGGTTGGAGTGGGCGGC -3'   2D8(+)
```

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

```
SEQ ID NO:68  5' Biotin- ATCATTCCAATCATCCATATCATC(A)25 -3' NH2   CYP(+)ran(A)25-5'Biotin,3'NH2
SEQ ID NO:69         5'- ATCATTCCAATCATCCATATCATC(A)25 -3' NH2   CYP(+)ran(A)25-3'NH2
```